

## Poster Abstract – P248

# Transmission of primary resistance mutation K103N in a cluster of Belgian young patients from different risk groups

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### Background

We analysed the distribution of an HIV-1 subtype B strain resistant to efavirenz and nevirapine among incident infections in the Belgian population.

### Method

The Belgian AIDS reference laboratories searched their databases for HIV-1 subtype B sequences harbouring the K103N mutation in the reverse transcriptase (RT) or the C67S and V77I mutations in the protease (PR). We included the earliest RT sequence available of drug-naïve patients as well as sequences related to treatment failure. Fifty sequences were aligned omitting the codon 103 and submitted to phylogenetic analysis. Epidemiological data were collected through the Institute of Public Health national database. In addition, three sequences from the cluster were analysed by deep sequencing using the Roche GS Junior platform.

### Results

Phylogenetic analysis revealed the presence of a 24 virus sequences cluster. All except one of those sequences resulted from patients who were ARV-naïve at the time of sampling, and 21 had the K103N mutation. Two thirds of the clustered patients were infected through homosexual or bisexual contacts while the others were heterosexuals. No case was related to migrants contaminated abroad. Fifteen of the clustered patients were diagnosed between January 2011 and June 2012; 87% of them were aged between 20 and 29 at the time of diagnosis. Interestingly, 60% of them reside in the province of Namur. Deep sequencing analysis of 3 individuals sampled near seroconversion revealed no other resistance mutations at a frequency > 1% than those already picked up by Sanger sequencing (RT A98S, K103N; PR V77I), except the RT V90I.

### Conclusion

We identified a transmission cluster of drug resistant HIV-1 variants mainly including homo- and heterosexual young adults. Most individuals are of Belgian origin and are living around the city of Namur (Belgium). The K103N mutation had no apparent impact on transmission fitness as its spread raised during the last years. These observations may impact on local prevention and ARV prophylaxis strategies.

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